

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 09/581,528E
Source: FW16
Date Processed by STIC: 2/3/05

ENTERED



IFW16

RAW SEQUENCE LISTING

DATE: 02/03/2005

PATENT APPLICATION: US/09/581,528E

TIME: 09:27:43

Input Set : A:\P19743.ST25.txt

Output Set: N:\CRF4\02032005\I581528E.raw

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3 <110> APPLICANT: TAKEDA, Masatoshi
4   TAKEDA, Junji
6 <120> TITLE OF INVENTION: Gene Mutant Animals
8 <130> FILE REFERENCE: P19743
10 <140> CURRENT APPLICATION NUMBER: 09/581,528E
11 <141> CURRENT FILING DATE: 2000-10-26
13 <150> PRIOR APPLICATION NUMBER: PCT/JP99/00015
14 <151> PRIOR FILING DATE: 1999-01-07
16 <160> NUMBER OF SEQ ID NOS: 22
18 <170> SOFTWARE: PatentIn version 3.3
20 <210> SEQ ID NO: 1
21 <211> LENGTH: 467
22 <212> TYPE: PRT
23 <213> ORGANISM: Human
25 <400> SEQUENCE: 1
27 Met Thr Glu Leu Pro Ala Asx Leu Ser Tyr Phe Gln Asn Ala Gln Met
28 1      5      10      15
31 Ser Glu Asp Asn His Leu Ser Asn Thr Val Arg Ser Gln Asn Asp Asn
32      20      25      30
35 Arg Glu Arg Gln Glu His Asn Asp Arg Arg Ser Leu Gly His Pro Glu
36      35      40      45
39 Pro Leu Ser Asn Gly Arg Pro Gln Gly Asn Ser Arg Gln Val Val Glu
40      50      55      60
43 Gln Asp Glu Glu Glu Asp Glu Glu Leu Thr Leu Lys Tyr Gly Ala Lys
44 65      70      75      80
47 His Val Ile Met Leu Phe Val Pro Val Thr Leu Cys Met Val Val Val
48      85      90      95
51 Val Ala Thr Ile Lys Ser Val Ser Phe Tyr Thr Arg Lys Asp Gly Gln
52      100     105     110
55 Leu Ile Tyr Thr Pro Phe Thr Glu Asp Thr Glu Thr Val Gly Gln Arg
56      115     120     125
59 Ala Leu His Ser Ile Leu Asn Ala Ala Ile Met Ile Ser Val Ile Val
60      130     135     140
63 Val Met Thr Ile Leu Leu Val Val Leu Tyr Lys Tyr Arg Cys Tyr Lys
64 145     150     155     160
67 Val Ile His Ala Trp Leu Ile Ile Ser Ser Leu Leu Leu Leu Phe Phe
68      165     170     175
71 Phe Ser Phe Ile Tyr Leu Gly Glu Val Phe Lys Thr Tyr Asn Val Ala
72      180     185     190
75 Val Asp Tyr Ile Thr Val Ala Leu Leu Ile Trp Asn Phe Gly Val Val
76      195     200     205
79 Gly Met Ile Ser Ile His Trp Lys Gly Pro Leu Arg Leu Gln Gln Ala
80      210     215     220

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83 Tyr Leu Ile Met Ile Ser Ala Leu Met Ala Leu Val Phe Ile Lys Tyr
84 225                230                235                240
87 Leu Pro Glu Trp Thr Ala Trp Leu Ile Leu Ala Val Ile Ser Val Tyr
88                245                250                255
91 Asp Leu Asp Ala Val Leu Cys Pro Lys Gly Pro Leu Arg Met Leu Val
92                260                265                270
95 Glu Thr Ala Gln Glu Arg Asn Glu Thr Leu Phe Pro Ala Leu Ile Tyr
96                275                280                285
99 Ser Ser Thr Met Val Trp Leu Val Asn Met Ala Glu Gly Asp Pro Glu
100                290                295                300
103 Ala Gln Arg Arg Val Ser Lys Asn Ser Lys Tyr Asn Ala Glu Ser Thr
104 305                310                315                320
107 Glu Arg Glu Ser Gln Asp Thr Val Ala Glu Asn Asp Asp Gly Gly Phe
108                325                330                335
111 Ser Glu Glu Trp Glu Ala Gln Arg Asp Ser His Leu Gly Pro His Arg
112                340                345                350
115 Ser Thr Pro Glu Ser Arg Ala Ala Val Gln Glu Leu Ser Ser Ser Ile
116                355                360                365
119 Leu Ala Gly Glu Asp Pro Glu Glu Arg Gly Val Lys Leu Gly Leu Gly
120                370                375                380
123 Asp Phe Ile Phe Tyr Ser Val Leu Val Gly Lys Ala Ser Ala Thr Ala
124 385                390                395                400
127 Ser Gly Asp Trp Asn Thr Thr Ile Ala Cys Phe Val Ala Ile Leu Ile
128                405                410                415
131 Gly Leu Cys Leu Thr Leu Leu Leu Leu Ala Ile Phe Lys Lys Ala Leu
132                420                425                430
135 Pro Ala Leu Pro Ile Ser Ile Thr Phe Gly Leu Val Phe Tyr Phe Ala
136                435                440                445
139 Thr Asp Tyr Leu Val Gln Pro Phe Met Asp Gln Leu Ala Phe His Gln
140                450                455                460
143 Phe Tyr Ile
144 465
147 <210> SEQ ID NO: 2
148 <211> LENGTH: 1404
149 <212> TYPE: DNA
150 <213> ORGANISM: Human
152 <400> SEQUENCE: 2
153 atgacagagt tacctgcacc gttgtcctac ttccagaatg cacagatgtc tgaggacaac      60
155 cacctgagca atactgtacg tagccagaat gacaatagag aacggcagga gcacaacgac      120
157 agacggagcc ttggccaccg tgagccatta tctaattgac gacccaggg taactcccgg      180
159 caggtggtgg agcaagatga ggaagaagat gaggagctga cattgaaata tggcgccaag      240
161 catgtgatca tgctctttgt ccctgtgact ctctgcatgg tgggtggtcgt ggctactatt      300
163 aagtcagtca gcttttatac ccggaaggat gggcagctaa tctatacccc attcacagaa      360
165 gataccgaga ctgtggggcca gagagccctg cactcaattc tgaatgctgc catcatgatc      420
167 agtgtcattg ttgtcatgac tatcctcctg gtggttctgt ataaatacag gtgctataag      480
169 gtcatccatg cctggcttat tatatcatct ctattgttgc tgttcttttt ttcattcatt      540
171 tacttggggg aagtgtttta aacctataac gttgctgtgg actacattac tgttgcactc      600
173 ctgatctgga attttggtgt ggtgggaatg atttccattc actggaaagg tccacttcga      660
175 ctccagcagg catatctcat tatgattagt gccctcatgg ccctggtgtt tatcaagtac      720

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177 ctccctgaat ggactgcgtg gctcatcttg gctgtgattt cagtatatga tttagtggct 780
179 gttttgtgtc cgaaagggtcc acttcgtatg ctgggtgaaa cagctcagga gagaaatgaa 840
181 acgctttttc cagctctcat ttactcctca acaatgggtg gggttggtgaa tatggcagaa 900
183 ggagaccgag aagctcaaag gagagtatcc aaaaattcca agtataatgc agaaagcaca 960
185 gaaagggagt cacaagacac tgttcagag aatgatgatg gcgggttcag tgaggaatgg 1020
187 gaagcccaga gggacagtca tctagggcct catcgctcta cacctgagtc acgagctgct 1080
189 gtccaggaac tttccagcag tatcctcgct ggtgaagacc cagaggaaa gggagtaaaa 1140
191 cttggattgg gagatttcat tttctacagt gttctgggtg gtaaagcctc agcaacagcc 1200
193 agtggagact ggaacacaac catagcctgt ttcgtagcca tattaattgg tttgtgcctt 1260
195 acattattac tccttgccat tttcaagaaa gcattgccag ctcttccaat ctccatcacc 1320
197 tttgggcttg ttttctactt tgccacagat tatcttgtag agccttttat ggaccaatta 1380
199 gcattccatc aattttatat ctag 1404

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202 <210> SEQ ID NO: 3

203 <211> LENGTH: 467

204 <212> TYPE: PRT

205 <213> ORGANISM: Mouse

207 <400> SEQUENCE: 3

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209 Met Thr Glu Ile Pro Ala Pro Leu Ser Tyr Phe Gln Asn Ala Gln Met
210 1 5 10 15
213 Ser Glu Asp Ser His Ser Ser Ser Ala Ile Arg Ser Gln Asn Asp Ser
214 20 25 30
217 Glu Glu Arg Gln Gln Gln His Asp Arg Gln Arg Leu Asp Asn Pro Glu
218 35 40 45
221 Pro Ile Ser Asn Gly Arg Pro Gln Ser Asn Ser Arg Gln Val Val Glu
222 50 55 60
225 Gln Asp Glu Glu Glu Asp Glu Glu Leu Thr Leu Lys Tyr Gly Ala Lys
226 65 70 75 80
229 His Val Ile Met Leu Phe Val Pro Val Thr Leu Cys Met Val Val Val
230 85 90 95
233 Val Ala Thr Ile Lys Ser Val Ser Phe Tyr Thr Arg Lys Asp Gly Gln
234 100 105 110
237 Leu Ile Tyr Thr Pro Phe Thr Glu Asp Thr Glu Thr Val Gly Gln Arg
238 115 120 125
241 Ala Leu His Ser Ile Leu Asn Ala Ala Ile Met Ile Ser Val Ile Val
242 130 135 140
245 Ile Met Thr Ile Leu Leu Val Val Leu Tyr Lys Tyr Arg Cys Tyr Lys
246 145 150 155 160
249 Val Ile His Ala Trp Leu Ile Ile Ser Ser Leu Leu Leu Phe Phe
250 165 170 175
253 Phe Ser Phe Ile Tyr Leu Gly Glu Val Phe Lys Thr Tyr Asn Val Ala
254 180 185 190
257 Val Asp Tyr Val Thr Val Ala Leu Leu Ile Trp Asn Phe Gly Val Val
258 195 200 205
261 Gly Met Ile Ala Ile His Trp Lys Gly Pro Leu Arg Leu Gln Gln Ala
262 210 215 220
265 Tyr Leu Ile Met Ile Ser Ala Leu Met Ala Leu Val Phe Ile Lys Tyr
266 225 230 235 240
269 Leu Pro Glu Trp Thr Ala Trp Leu Ile Leu Ala Val Ile Ser Val Tyr
270 245 250 255

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273 Asp Leu Val Ala Val Leu Cys Pro Lys Gly Pro Leu Arg Met Leu Val
 274 260 265 270
 277 Glu Thr Ala Gln Glu Arg Asn Glu Thr Leu Phe Pro Ala Leu Ile Tyr
 278 275 280 285
 281 Ser Ser Thr Met Val Trp Leu Val Asn Met Ala Glu Gly Asp Pro Glu
 282 290 295 300
 285 Ala Glu Arg Arg Val Pro Lys Asn Pro Lys Tyr Asn Thr Gln Arg Ala
 286 305 310 315 320
 289 Glu Arg Glu Thr Gln Asp Ser Gly Ser Gly Asn Asp Asp Gly Gly Phe
 290 325 330 335
 293 Ser Glu Glu Trp Glu Ala Gln Arg Asp Ser His Leu Gly Pro His Arg
 294 340 345 350
 297 Ser Thr Pro Glu Ser Arg Ala Ala Val Gln Glu Leu Ser Gly Ser Ile
 298 355 360 365
 301 Leu Thr Ser Glu Asp Pro Glu Glu Arg Gly Val Lys Leu Gly Leu Gly
 302 370 375 380
 305 Asp Phe Ile Phe Tyr Ser Val Leu Val Gly Lys Ala Ser Ala Thr Ala
 306 385 390 395 400
 309 Ser Gly Asp Trp Asn Thr Thr Ile Ala Cys Phe Val Ala Ile Leu Ile
 310 405 410 415
 313 Gly Leu Cys Leu Thr Leu Leu Leu Leu Ala Ile Phe Lys Lys Ala Leu
 314 420 425 430
 317 Pro Ala Leu Pro Ile Ser Ile Thr Phe Gly Leu Val Phe Tyr Phe Ala
 318 435 440 445
 321 Thr Asp Tyr Leu Val Gln Pro Phe Met Asp Gln Leu Ala Phe His Gln
 322 450 455 460
 325 Phe Tyr Ile
 326 465

329 <210> SEQ ID NO: 4

330 <211> LENGTH: 1404

331 <212> TYPE: DNA

332 <213> ORGANISM: Mouse

334 <400> SEQUENCE: 4

335	atgacagaga	tacctgcacc	tttgtcctac	ttccagaatg	cccagatgtc	tgaggacagc	60
337	cactccagca	gcgccatccg	gagccagaat	gacagccaag	aacggcagca	gcagcatgac	120
339	aggcagagac	ttgacaaccc	tgagccaata	tctaattggc	ggccccagag	taactcaaga	180
341	caggtggtgg	aacaagatga	ggaggaagac	gaagagctga	cattgaaata	tgagaccaag	240
343	catgtcatca	tgctctttgt	ccccgtgacc	ctctgcatgg	tcgtcgtcgt	ggccaccatc	300
345	aaatcagtca	gcttctatac	ccggaaggac	ggtcagctaa	tctacacccc	attcacagaa	360
347	gacactgaga	ctgtaggcca	aagagccctg	cactcgatcc	tgaatgcggc	catcatgac	420
349	agtgtcattg	tcattatgac	catcttcctg	gtggctcctg	ataaatacag	gtgtacaag	480
351	gtcatccacg	cctggccttat	tatttcattc	ctgttggtgc	tggtcttttt	ttcgttcatt	540
353	tacttagggg	aagtatttaa	gacctacaat	gtcgccgtgg	actacgttac	agtagcactc	600
355	ctaactctga	attttggtgt	ggtcgggatg	attgccatcc	actggaaagg	cccccttcga	660
357	ctgcagcagg	cgtatctcat	tatgatcagt	gccctcatgg	ccctggtatt	tatcaagtac	720
359	ctccccgaat	ggaccgcatg	gctcatcttg	gctgtgattt	cagtatatga	tttggtggct	780
361	gttttatgtc	ccaaaggccc	acttcgtatg	ctgggtgaaa	cagctcagga	aagaaatgag	840
363	actctctttc	cagctcttat	ctattcctca	acaatgggtg	ggttggtgaa	tatggctgaa	900
365	ggagacccag	aagcccaaag	gagggtaccc	aagaacccca	agtataacac	acaaagagcg	960

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367 gagagagaga cacaggacag tgggttctggg aacgatgatg gtggcttcag tgaggagtgg 1020
369 gaggcccaaa gagacagtca cctggggcct catcgctcca ctcccagatc aagagctgct 1080
371 gtccaggaac tttctgggag cattctaacg agtgaagacc cggaggaaag aggagtaaaa 1140
373 cttggactgg gagatttcat tttctacagt gttctgggtg gtaaggcctc agcaaccgcc 1200
375 agtggagact ggaacacaac catagcctgc tttgtagcca tactgatcgg cctgtgcctt 1260
377 acattactcc tgctcgccat tttcaagaaa gcgttgccag ccctcccat ctccatcacc 1320
379 ttcgggctcg tgttctactt cgccacggat taccttgtgc agcccttcat ggaccaactt 1380
381 gcattccatc agttttatat ctac                                     1404
384 <210> SEQ ID NO: 5
385 <211> LENGTH: 25
386 <212> TYPE: DNA
387 <213> ORGANISM: Artificial
389 <220> FEATURE:
390 <223> OTHER INFORMATION: Primer
392 <400> SEQUENCE: 5
393 ggaatttttg tgtggtcggg atgat                                     25
396 <210> SEQ ID NO: 6
397 <211> LENGTH: 23
398 <212> TYPE: DNA
399 <213> ORGANISM: Artificial
401 <220> FEATURE:
402 <223> OTHER INFORMATION: Primer
404 <400> SEQUENCE: 6
405 ggtccattcg gggaggtact tga                                     23
408 <210> SEQ ID NO: 7
409 <211> LENGTH: 36
410 <212> TYPE: DNA
411 <213> ORGANISM: Artificial
413 <220> FEATURE:
414 <223> OTHER INFORMATION: Primer
416 <400> SEQUENCE: 7
417 tgtggtcggg atgatcgcca ccactggaa aggccc                                     36
420 <210> SEQ ID NO: 8
421 <211> LENGTH: 36
422 <212> TYPE: DNA
423 <213> ORGANISM: Artificial
425 <220> FEATURE:
426 <223> OTHER INFORMATION: Primer
428 <400> SEQUENCE: 8
429 gggcctttcc agtgggtggc gatcatcccg accaca                                     36
432 <210> SEQ ID NO: 9
433 <211> LENGTH: 18
434 <212> TYPE: DNA
435 <213> ORGANISM: Artificial
437 <220> FEATURE:
438 <223> OTHER INFORMATION: Primer
440 <400> SEQUENCE: 9
441 tctagacggc cgtctaga                                     18
444 <210> SEQ ID NO: 10

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RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/09/581,528E

DATE: 02/03/2005
TIME: 09:27:44

Input Set : A:\P19743.ST25.txt
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Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:5,6,7,8,9,10,11,12,13,14,15,16,17,18,19,20,21,22

VERIFICATION SUMMARY

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